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Figure 1A  
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1 ATGAGCTCCGCGATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60  
1 M S S R I A R A L A L V V T L L H L T R 20

61 CTGGCGCTCTCCACCTGCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGC GCG 120  
21 L A L S T C P A A C H C P L E A P K C A 40

121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGCTCGGCCAAGCAGCTC 180  
41 P G V G L V R D G C G C C K V C A K Q L 60

181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240  
61 N E D C S K T Q P C D H T K G L E C N F 80

241 GGGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCGTG 300  
81 G A S S T A L K G I C R A Q S E G R P C 100

301 GAATATAACTCCAGAATCTACCAAAACGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360  
101 E Y N S R I Y Q N G E S F Q P N C K H Q 120

361 TGCACATGTATTGATGGCGCGTGGGCTGCATTCTCTGTGTCCCCAAGAACTATCTCTC 420  
121 C T C I D G A V G C I P L C P Q E L S L 140

421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480  
141 P N L G C P N P R L V K V T G Q C C E E 160

481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540  
161 W V C D E D S I K D P M E D Q D G L L G 180

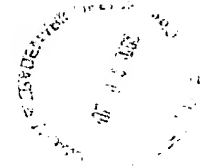
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181 K E L G F D A S E V E L T R N N E L I A 200

601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTGGAATGGAGCCTCGCATCCTA 660  
201 V G K G S S L K R L P V F G M E P R I L 220

661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACCTTATGGTCCCAGTGCTCA 720  
221 Y N P L Q G Q K C I V Q T T S W S Q C S 240

721 AAGACCTGTGGAAGTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCTT 780  
241 K T C G T G I S T R V T N D N P E C R L 260

781 GTGAAAGAAACCCGATTGTTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840  
261 V K E T R I C E V R P C G Q P V Y S S L 280

**Figure 1B**

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|      |  |      |
|------|--|------|
| 841  | AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGAACCAGTCAGGTTTACTTAC    | 900  |
| 281  | K K G K K C S K T K K S P E P V R F T Y                        | 300  |
| 901  | GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCTTGCGTGGACGGC   | 960  |
| 301  | A G C L S V K K Y R P K Y C G S C V D G                        | 320  |
| 961  | CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG   | 1020 |
| 321  | R C C T P Q L T R T V K M R F R C E D G                        | 340  |
| 1021 | GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAAATGCAACTACAAC TGCCCG | 1080 |
| 341  | E T F S K N V M M I Q S C K C N Y N C P                        | 360  |
| 1081 | CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG   | 1140 |
| 361  | H A N E A A F P F Y R L F N D I H K F R                        | 380  |
| 1141 | GACTAA   | 1146 |
| 381  | D *  | 382  |

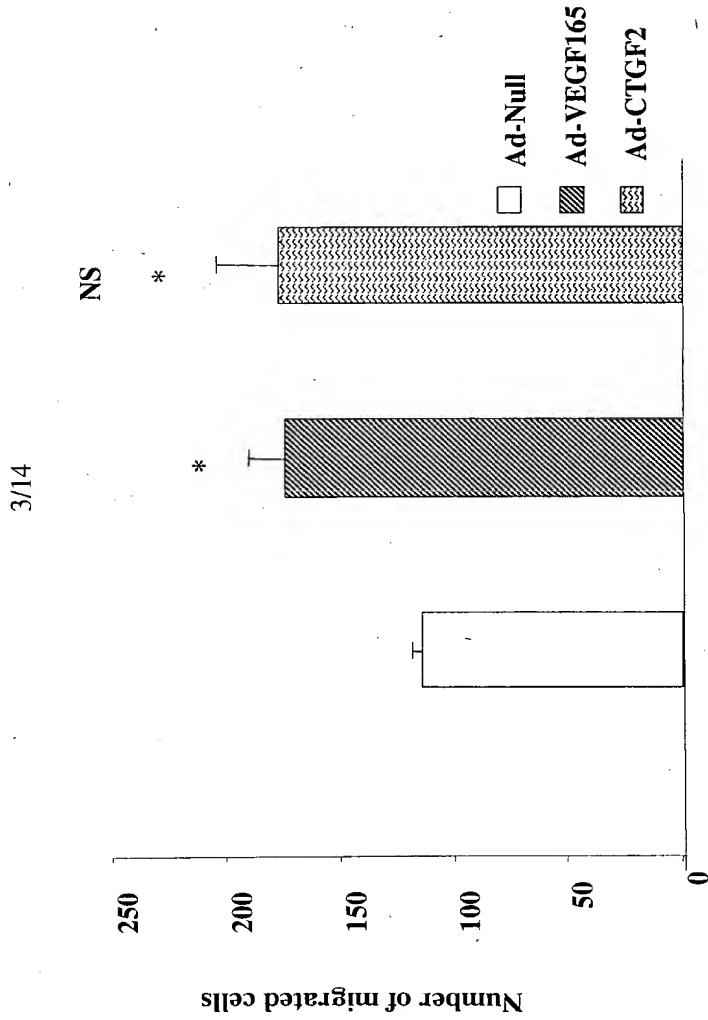
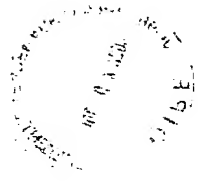


Figure 2

Figure 3

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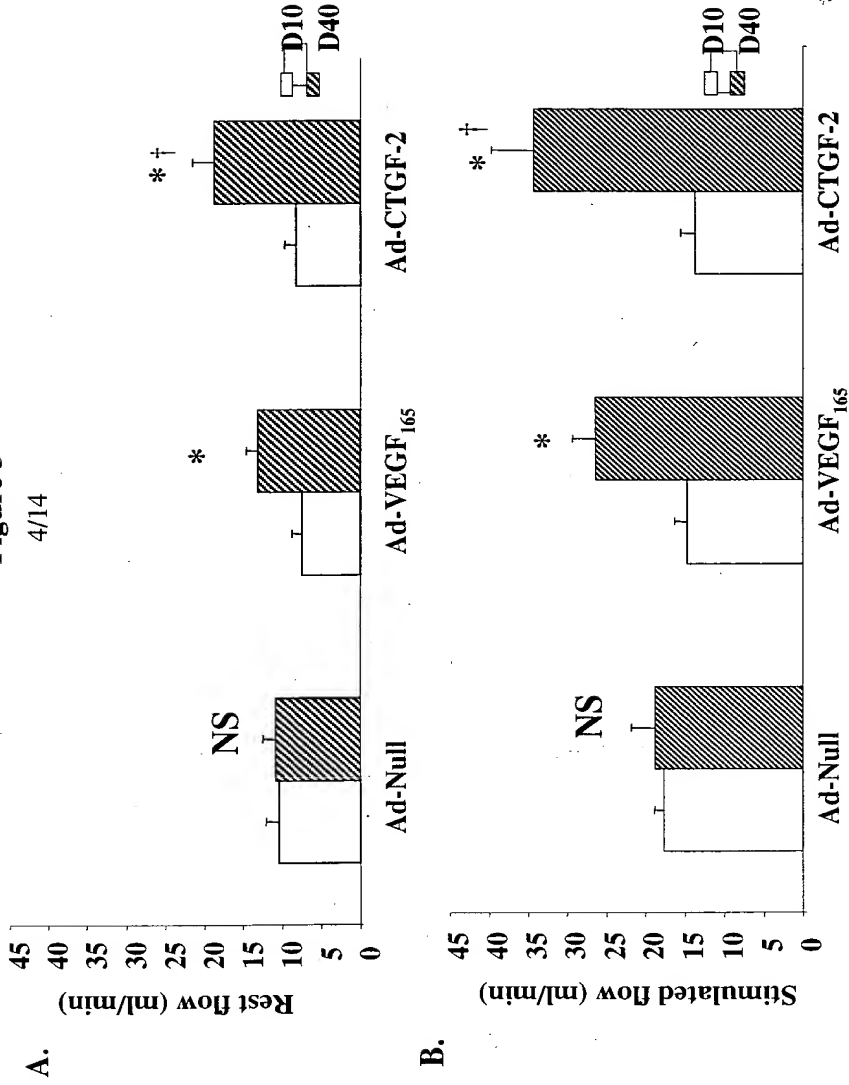
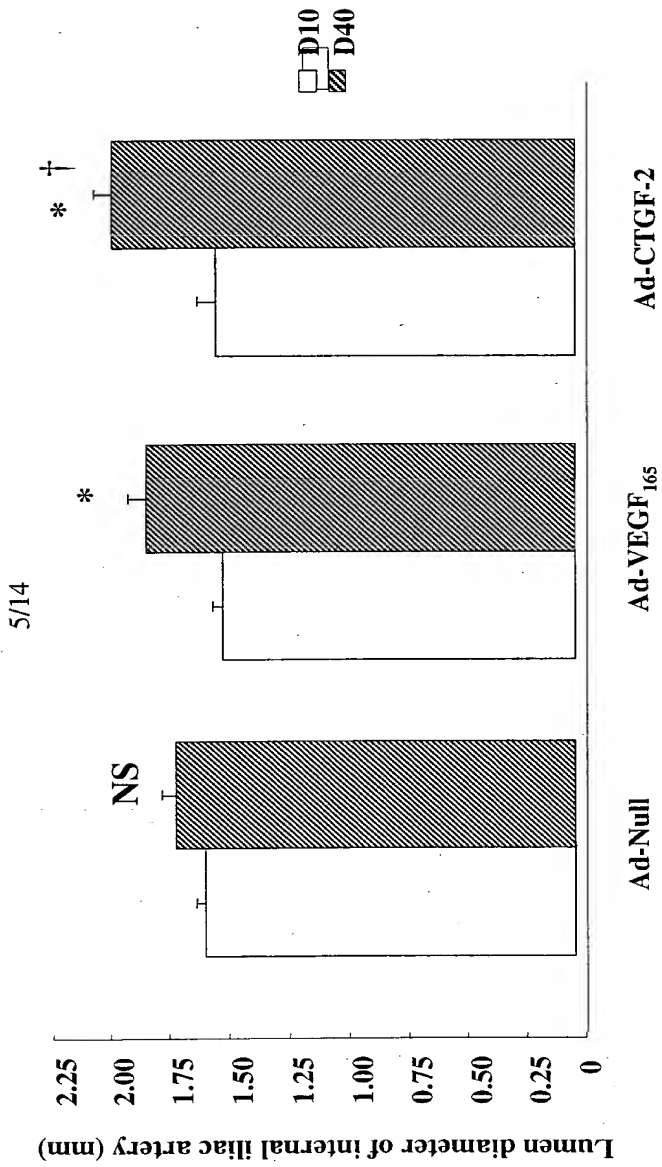


Figure 4



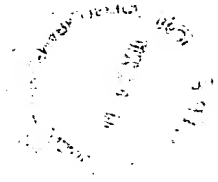
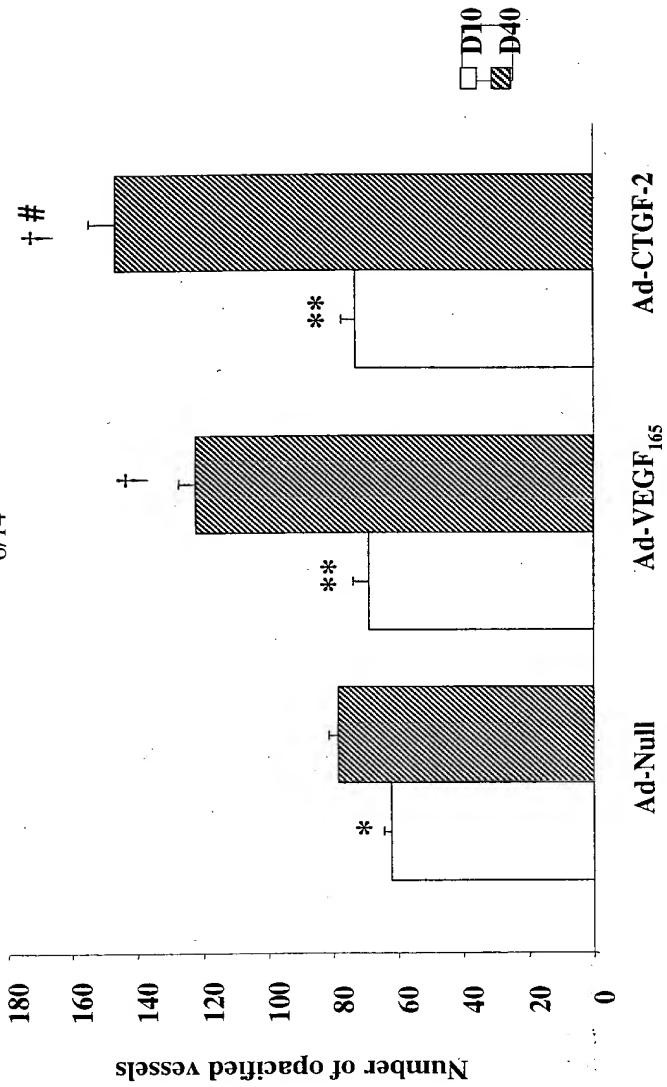


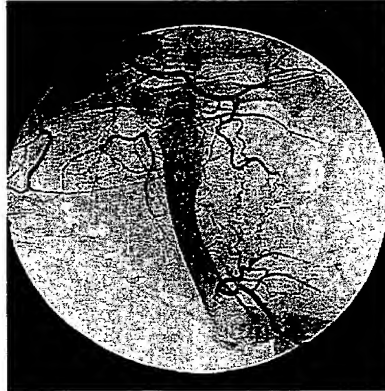
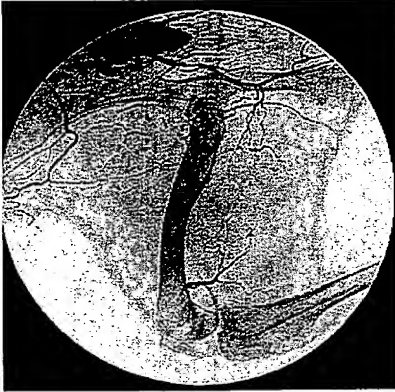
Figure 5

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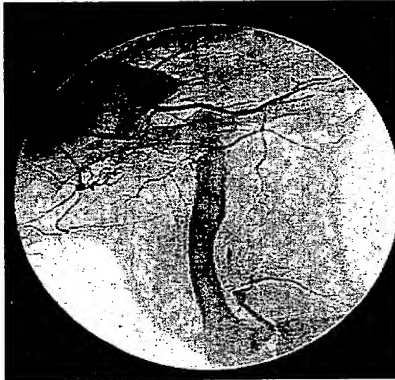


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Ad-CTGF2



Ad-VEGF165



Ad-Null

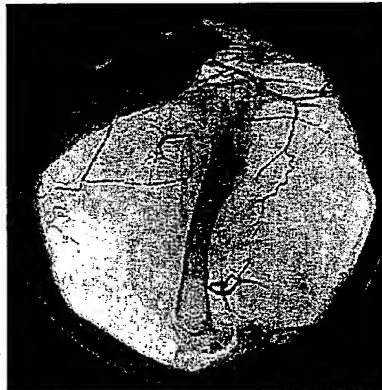
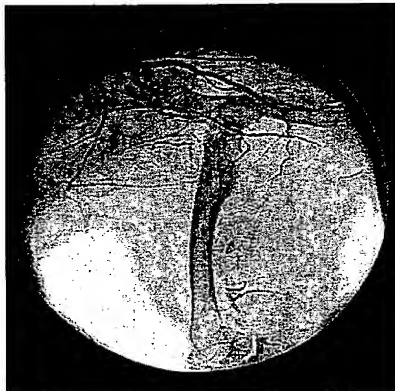
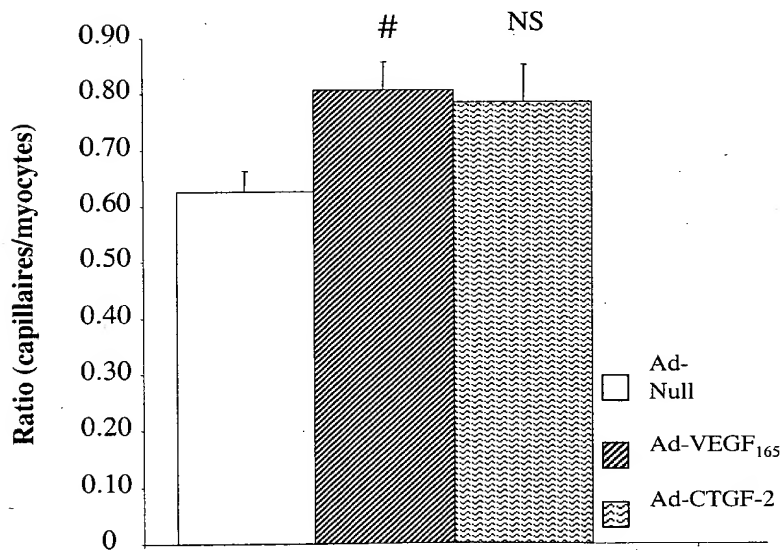
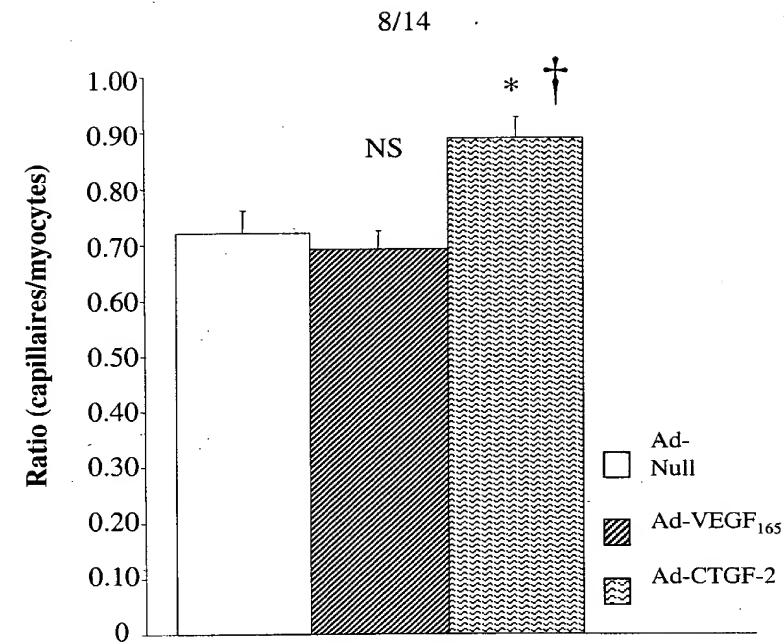


Figure 6



**Figure 7**

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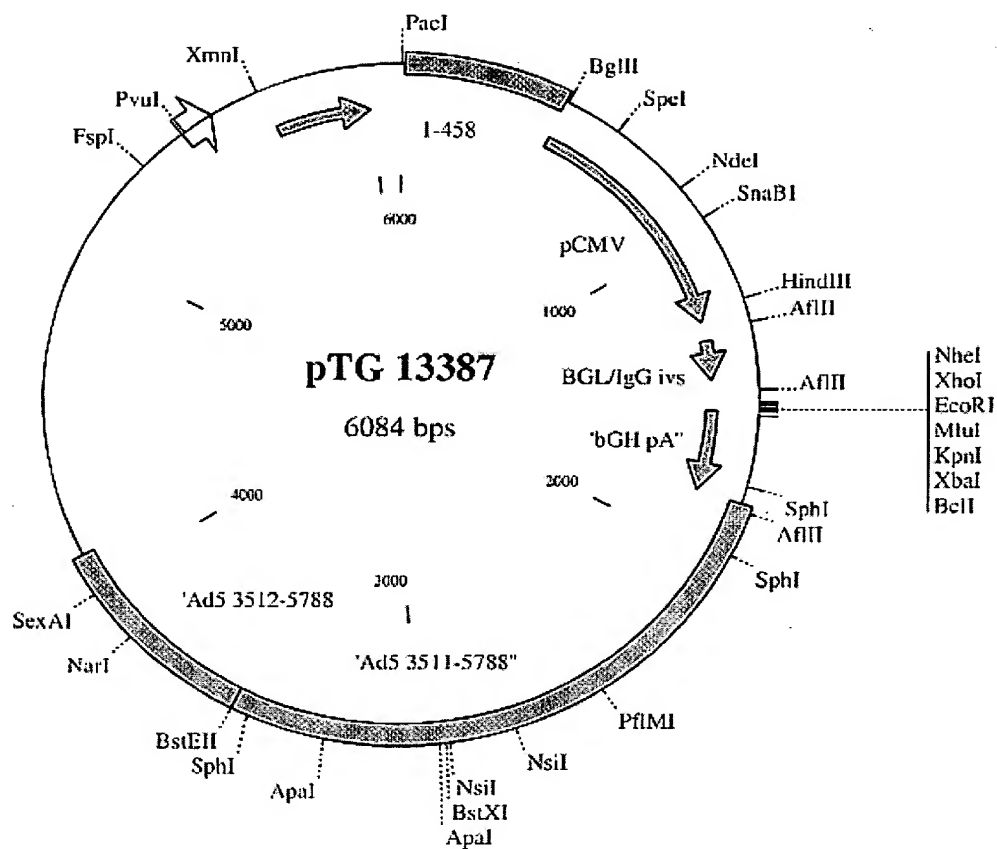


Figure 8

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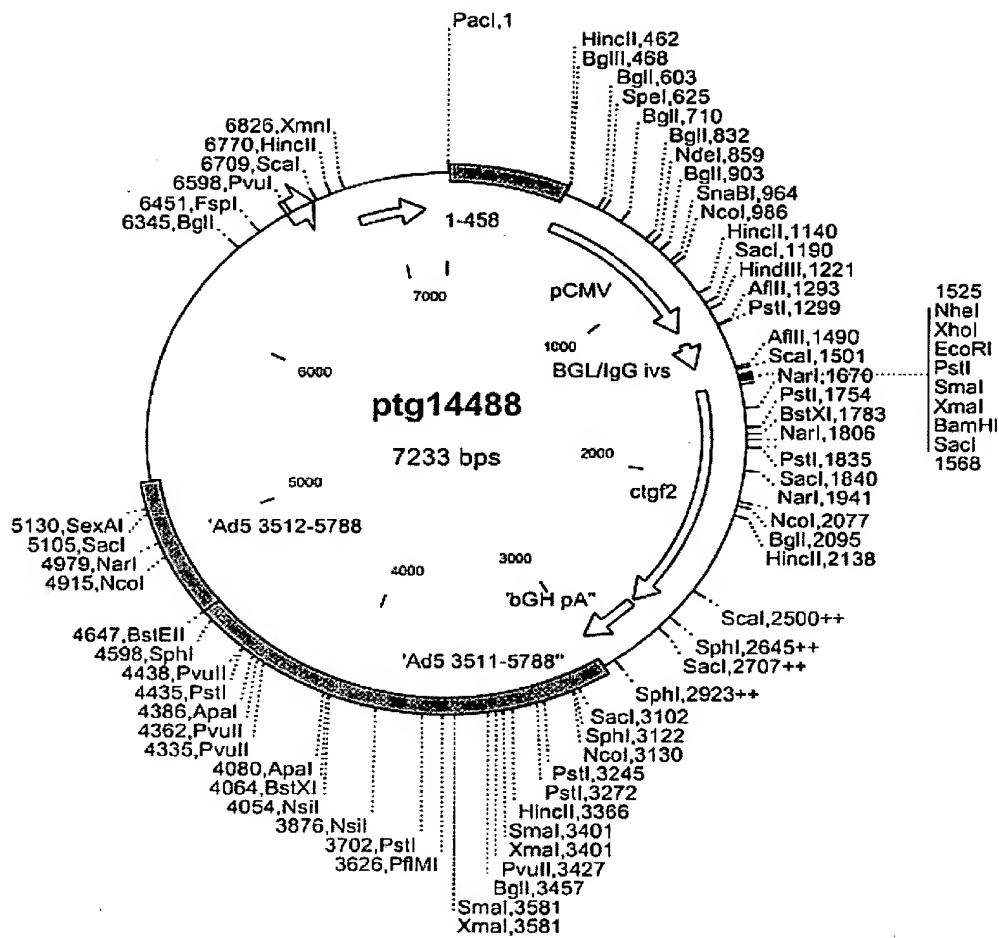


Figure 9

Figure 10  
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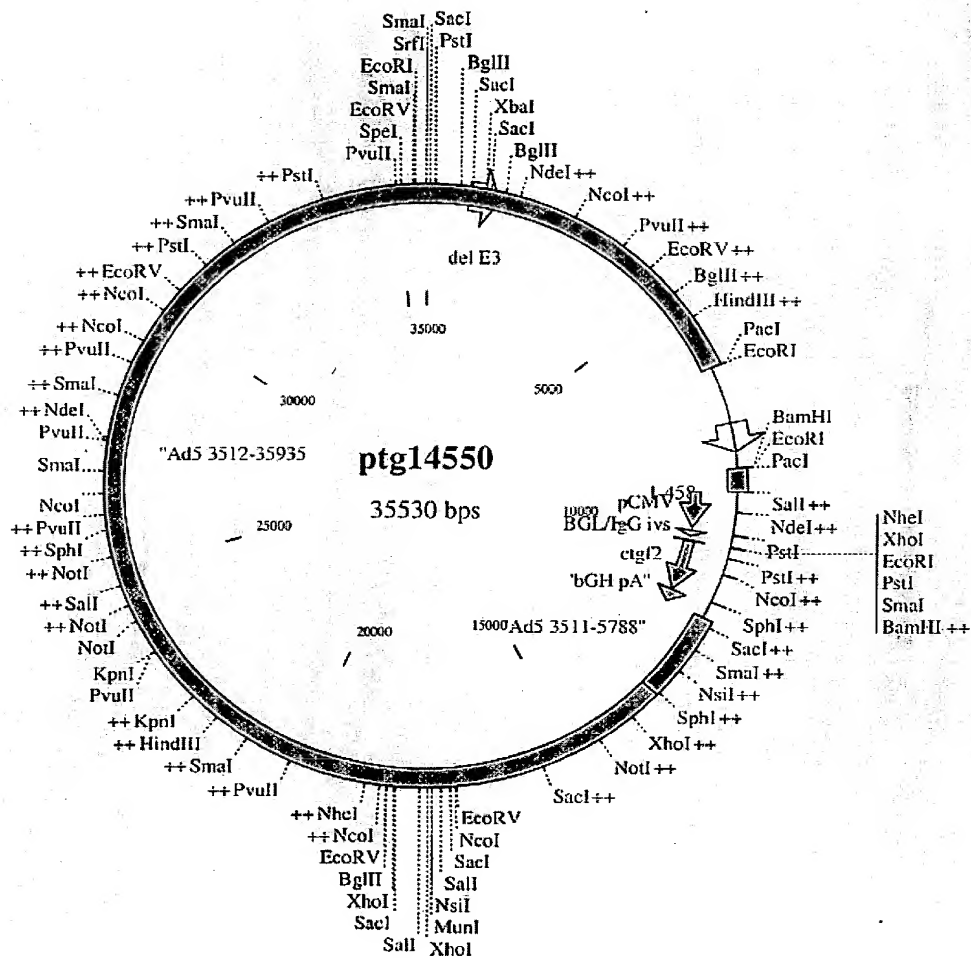


Figure 11A  
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ATGAGCTCCCGAATCGTCAGGAGCTCGCTTAGTCGTCACCCCTTCTCCACTTGCACAGG  
M S S R I V R E L A L V V T L L H L T R

GTGGGGCTCTCCACTGCCCCCTGACTGCCACTGCCCCCTGGAGGGCGCCCAAGTGGCG  
V G L S T C P A D C H C P L E A P K C A

CCGGGACTCGGGCTGGTCCGGGACGGCTGCGGGCTGTTGTAAGGTCTGCGCCAAAGCAGCTC  
P G V G L V R D G C C C K V C A K Q L

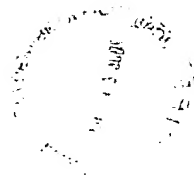
AACGAGGACTGCAGAAAACGCGAGCCCTGCGACCACACCAAGGGGCTGGAATGCACTTC  
N E D C R K T Q P C D H T K G L E C N F

GGCGCCAGCTCCACGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCGACACCCCTGT  
G A S S T A L K G I C R A Q S E G R P C

GAATATACTCCAGAATCTACCAAAACGGGGAAAGTTTCAGGCCCAACTGTAAACATCAG  
E Y N S R I Y Q N G E S F Q P N C K H Q

TGCACATGTATTGGATGGCGGGGGCTTGCATTCTCTGTGTCTCCCAAGAACTATCT  
C T C I G W R R G A C I P L C P Q E L S

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**Figure 11C**  
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CTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGGAACCAAGTCAGGTTTACT  
L K K G K K C S K T K K S P E P V R F T

TACGCTGGATGTTTGAGTGTGAAGAAATACGGCCCAAGTACTGCGGTTCTCTGCGTGGAC  
Y A G C L S V K K Y R P K Y C G S C V D

GGCCGATGCTGCACGCCCCAGCTGACCAAGGACTGTGAAGATGCGGTCCCTGCGAAGAT  
G R C C C T P O L T R T V K M R F P C E D

GGGGAGACATTTTCCAAAGAACGTTCATGATGATCCAGTCTCTCCAAATGCAACTACAACTGC  
G E T F S K N V M M I Q S S K C N Y N C

CCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCCAATGA  
P H A N E A A F P F Y R L E Q .

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